Resource Summary Report

Generated by NIF on Apr 27, 2025

HiC-Pro

RRID:SCR_017643
Type: Tool

Proper Citation

HiC-Pro (RRID:SCR_017643)

Resource Information

URL: https://github.com/nservant/HiC-Pro

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Description: Software tool as optimized and flexible pipeline for Hi-C data processing. Used to process Hi-C data, from raw fastq files, paired end Illumina data, to normalized contact maps.

Resource Type: data processing software, software resource, workflow software, software application

Defining Citation: PMID:26619908

Keywords: Hi-C, data, raw, fastq, file, paired, Illumina, normalized, contact, map, bio.tools

Funding: France Genomique National infrastructure ;
Labex Deep ;
European Research Coucil ;
ERC Advanced Investigator award ;
European Commission ;
ABS4NGS project ;
National Human Genome Research Institute ;
Paris Alliance of Cancer Research Institutes ;
Howard Hughes Medical Institute

Availability: Free, Available for download, Freely available

Resource Name: HiC-Pro

Resource ID: SCR_017643

Alternate IDs: biotools:hic-pro

Alternate URLs: https://bio.tools/hic-pro

License: BSD-3 Licence

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250426T060634+0000

Ratings and Alerts

No rating or validation information has been found for HiC-Pro.

No alerts have been found for HiC-Pro.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 166 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Guan DL, et al. (2025) A high-quality chromosome-level genome assembly of the mulberry looper, Phthonandria atrilineata. Scientific data, 12(1), 186.

Wang Z, et al. (2025) A high-quality assembly revealing the PMEL gene for the unique plumage phenotype in Liancheng ducks. GigaScience, 14.

Li N, et al. (2025) Chromosome-scale genome assembly of three-spotted seahorse (Hippocampus trimaculatus) with a unique karyotype. Scientific data, 12(1), 49.

Liu S, et al. (2025) Chromosome-level genome assembly and annotation of Japanese anchovy (Engraulis japonicus). Scientific data, 12(1), 134.

Liu Y, et al. (2025) Reference genome provide insights into sex determination of silver aworana (Osteoglossum bicirrhosum). BMC biology, 23(1), 29.

Cheng Y, et al. (2024) Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. Journal of advanced research, 56, 15.

Zhao Y, et al. (2024) Accelerating 3D genomics data analysis with Microcket. Communications biology, 7(1), 675.

Chen B, et al. (2024) Stratifying TAD boundaries pinpoints focal genomic regions of regulation, damage, and repair. Briefings in bioinformatics, 25(4).

Banerjee D, et al. (2024) Lineage specific transcription factor waves reprogram neuroblastoma from self-renewal to differentiation. Nature communications, 15(1), 3432.

Li X, et al. (2024) The first chromosome-level genome of the stag beetle Dorcus hopei Saunders, 1854 (Coleoptera: Lucanidae). Scientific data, 11(1), 396.

Wang YS, et al. (2024) Chromosome-level genome assemblies of two littorinid marine snails indicate genetic basis of intertidal adaptation and ancient karyotype evolved from bilaterian ancestors. GigaScience, 13.

Florez-Vargas O, et al. (2024) Genetic regulation of TERT splicing contributes to reduced or elevated cancer risk by altering cellular longevity and replicative potential. medRxiv : the preprint server for health sciences.

Ginley-Hidinger M, et al. (2024) Cis-regulatory control of transcriptional timing and noise in response to estrogen. Cell genomics, 4(5), 100542.

Fan H, et al. (2024) Chromosome-scale genome assembly of Astragalus membranaceus using PacBio and Hi-C technologies. Scientific data, 11(1), 1071.

Zhou Y, et al. (2024) Integration of scHi-C and scRNA-seq data defines distinct 3D-regulated and biological-context dependent cell subpopulations. Nature communications, 15(1), 8310.

Yuan L, et al. (2024) The genomes of 5 underutilized Papilionoideae crops provide insights into root nodulation and disease resistance. GigaScience, 13.

Zhang H, et al. (2024) The High-Quality Genome Sequencing and Analysis of Red Raspberry (Rubus idaeus L.). International journal of genomics, 2024, 9271183.

He C, et al. (2024) A chromosome-scale reference genome assembly for Triplophysa lixianensis. Scientific data, 11(1), 1404.

Feng L, et al. (2024) A reference-grade genome of the xerophyte Ammopiptanthus mongolicus sheds light on its evolution history in legumes and drought-tolerance mechanisms. Plant communications, 5(7), 100891.

Wang Y, et al. (2024) Chromosome-scale genome, together with transcriptome and metabolome, provides insights into the evolution and anthocyanin biosynthesis of Rubus rosaefolius Sm. (Rosaceae). Horticulture research, 11(4), uhae064.